FIGURE 1

```
ctgagatttt acttgaaatg aaggcgaggg cctgataggt tatgatttgc aaagagcgtg 61
ggttcaggat catttgtctg tactgtaaag tgttattagc gctaatattt cgcttcaggt 121
aaaagagggg cgtgcgccac aggtgctgga gacggggagc gcctttccgc tgctggagaa 181
acgcacgcac attcacctgc agcaaaacaa gctttccagg taaatgatgt ctcgtgatac 241
taaaacagag tcgcaacaat ctcagggcac ttcaagttcc tcgtcctcca gtgctcctca 301
atcttacagt cagtcgtctt catcgggtac attaagttct ttggatactg ttccagtgca 361
agatcttgcg tccattcctg aagaccctga gatagacgag gatatacccc agccttgggg 421
tcgtctctgg gctcttggga agggctttct aaatcatgat tgcctgcatg aagaatatgt 481
atttggaaga gacaaaaaat gtgattacac ctttgatatt ccagtactaa accagaccga 541
caggtacaaa acatatagca aaaggcactt cagaatattt caggaattag gtcatggaca 601
ctcccgtgtt gctaacatag aagatctgag cggcaacgga acatttgtta acaaggagat 661
tattggaaaa gggcggacat tgcctttaac aaataatgcc gagattgcac tttcattacc 721
aactaataaa gtttttgttt tttcagattt gtctgtggat gatcagacta tatatcctaa 781
ggacttcatt gataaataca tcatgtcaag gccaatcgga agtggggctt gcggggaagt 841
gaaattggct tttcaaaagt cagtatgcaa gaaggttgct gtaaaaatca tcagtaaaag 901
aaaatttaaa atgaacactt ctagtaatga acaccctata tctgttgaca cagaaataga 961
gatcctgaaa aaacttgatc atccctgtat cattaaaata gagaattttt ttgactctga 1021
ggacttctat tacattgtgt tggaactgat ggaaggaggc gaactgtttg acagggtggt 1081
aaattcgaca agactccgag aaccaattgc caaactgtat ttttatcaga tgctgctagc 1141
tgttcagtac ctccatgaaa atggggtgat acatcgtgat ctgaagcctg aaaatgtgct 1201
gttgtcatcc actagtgaag aatgttgcat aaagataacg gattttggac agtcaaaaat 1261
tctgggtgaa acgtctttaa tgagaacttt gtgtggaact cctacatact tggcgcctga 1321
agttttgaat acagcaggca caactggata cagtagtgca gtggattgct ggagtttagg 1381
agtcatcctt tttgtgtgtc tttgtggata tccccccttt tcagaacaaa atagtaacat 1441
tcccttgaaa aatcagattg cagagggaaa atacacctac attgctgctg cttggagaaa 1501
tgtatcagaa caagcatttg atttagtcaa gaatcttctt gttgttgatc ctgagcaaag 1561
acttaccact aaacaagcac tggaacatcc ctggcttcag gacgattcta tgaagcatac 1621
tgttgaaagg ttaatgtatg gggttgacca cacaatgcct cctccaatca agaaaaacat 1681
aattcgaaaa cggggacatg aatgggatca agatgccagt acttcatctt gctcagagat 1741
attaccaaca tcagccgaaa agagagcaaa aagataaaac aaaaaaaata cattgcgctt 1801
tatttaataa atgtttttgt aaaaaaaaaa aaaaaaaaaa aaaaa
```

FIGURE 2

```
MMSRDTKTES QQSQGTSSSS SSSAPQSYSQ SSSSGTLSSL DTVPVQDLAS IPEDPEIDED 61
IPQPWGRLWA LGKGFLNHDC LHEEYVFGRD KKCDYTFDIP VLNQTDRYKT YSKRHFRIFQ 121
ELGHGHSRVA NIEDLSGNGT FVNKEIIGKG RTLPLTNNAE IALSLPTNKV FVFSDLSVDD 181
QTIYPKDFID KYIMSRPIGS GACGEVKLAF QKSVCKKVAV KIISKRKFKM NTSSNEHPIS 241
VDTEIEILKK LDHPCIIKIE NFFDSEDFYY IVLELMEGGE LFDRVVNSTR LREPIAKLYF 301
YQMLLAVQYL HENGVIHRDL KPENVLLSST SEECCIKITD FGQSKILGET SLMRTLCGTP 361
TYLAPEVLNT AGTTGYSSAV DCWSLGVILF VCLCGYPPFS EQNSNIPLKN QIAEGKYTYI 421
AAAWRNVSEQ AFDLVKNLLV VDPEQRLTTK QALEHPWLQD DSMKHTVERL MYGVDHTMPP 481
PIKKNIIRKR GHEWDQDAST SSCSEILPTS AEKRAKR
```

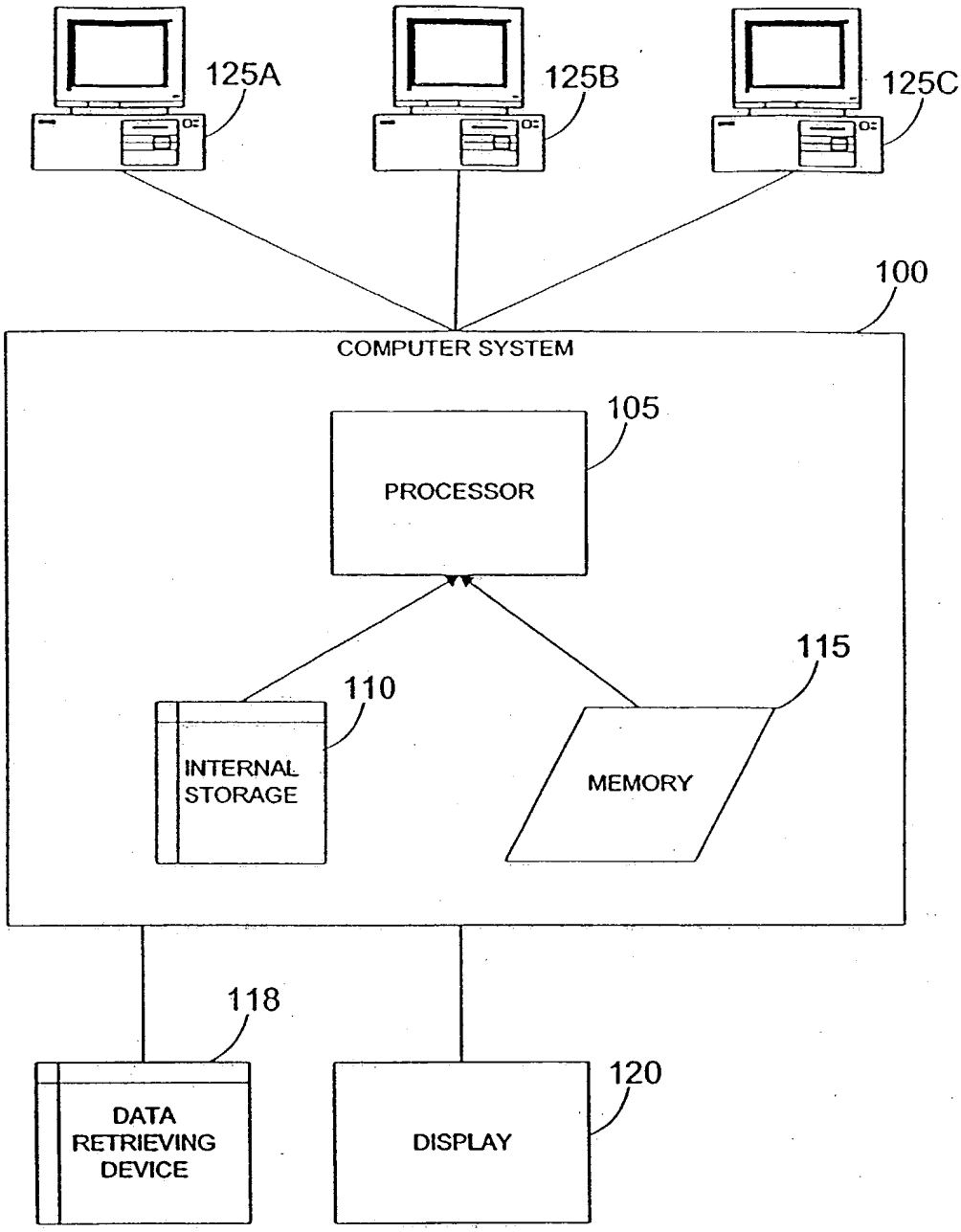
125A
125B
125C
100
COMPUTER SYSTEM
105
PROCESSOR
115
110
INTERNAL STORAGE
MEMORY
118
DATA RETRIEVING DEVICE
120
DISPLAY

FIGURE 3

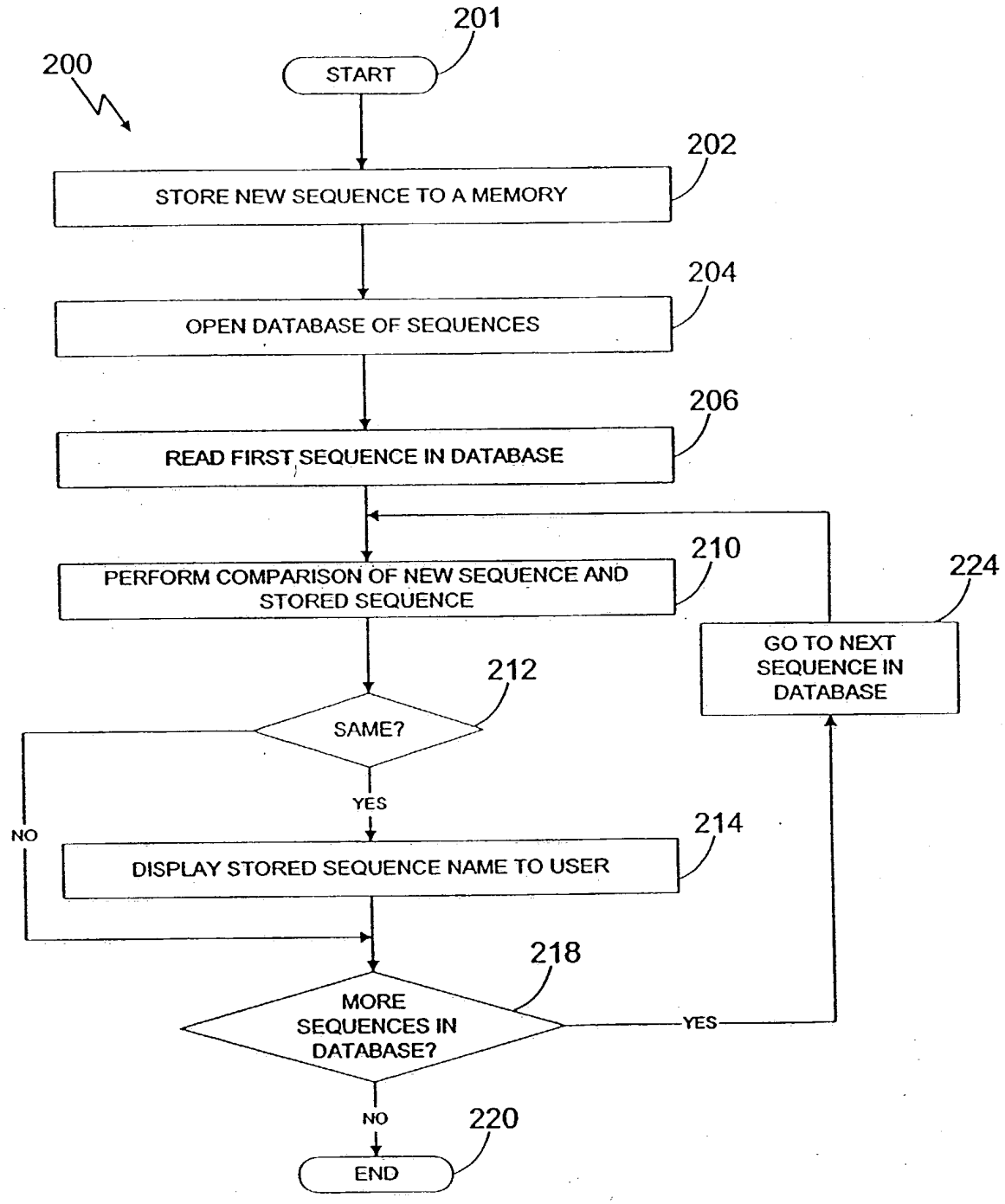
200
201
START
202
STORE NEW SEQUENCE TO A MEMORY
204
OPEN DATABASE OF SEQUENCES
206
READ FIRST SEQUENCE IN DATABASE
210
PERFORM COMPARISON OF NEW SEQUENCE AND STORED SEQUENCE
212
SAME?
YES
NO
214
DISPLAY STORED SEQUENCE NAME TO USER
218
MORE SEQUENCES IN DATABASE?
YES
NO
220
END
224
GO TO NEXT SEQUENCE IN DATABASE

FIGURE 4

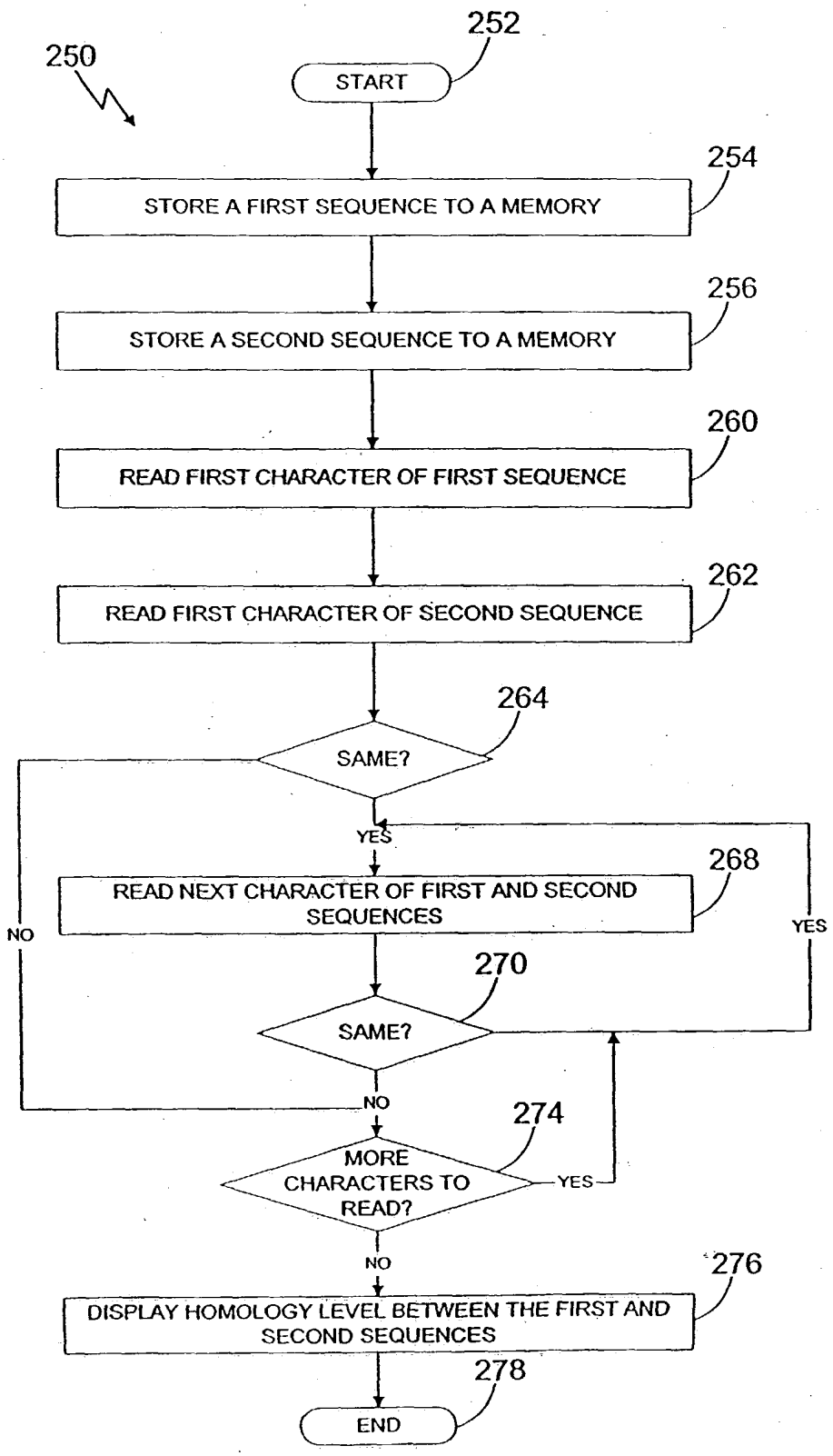
250
252
START
254
STORE A FIRST SEQUENCE TO A MEMORY
256
STORE A SECOND SEQUENCE TO A MEMORY
260
READ FIRST CHARACTER OF FIRST SEQUENCE
262
READ FIRST CHARACTER OF SECOND SEQUENCE
264
SAME?
YES
NO
268
READ NEXT CHARACTER OF FIRST AND SECOND SEQUENCES
YES
270
SAME?
NO
274
MORE CHARACTERS TO READ?
YES
NO
276
DISPLAY HOMOLOGY LEVEL BETWEEN THE FIRST AND SECOND SEQUENCES
278
END

FIGURE 5

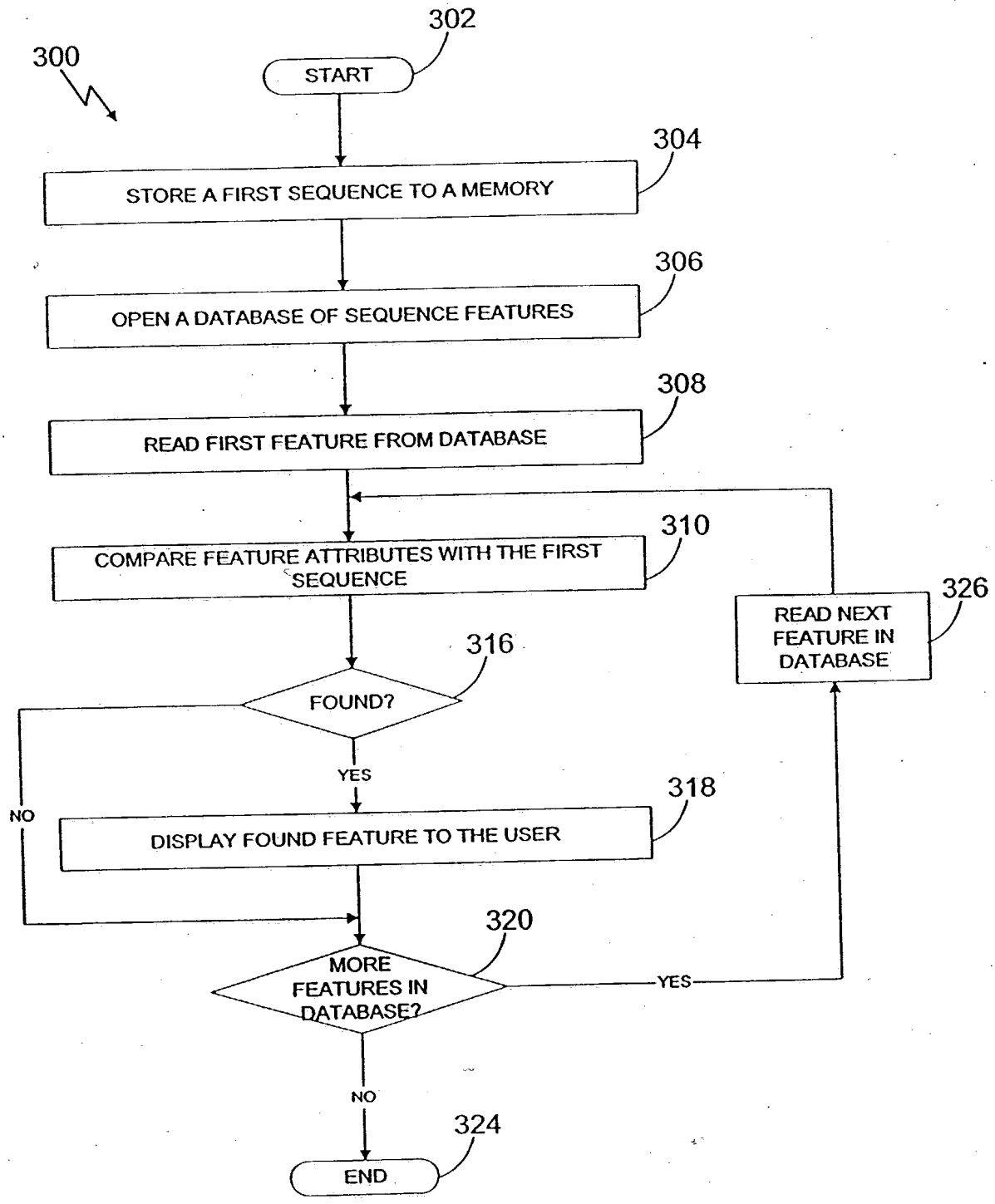
300
302
START
304
STORE A FIRST SEQUENCE TO A MEMORY
306
OPEN A DATABASE OF SEQUENCE FEATURES
308
READ FIRST FEATURE FROM DATABASE
310
COMPARE FEATURE ATTRIBUTES WITH THE FIRST SEQUENCE
316
FOUND?
YES
NO
318
DISPLAY FOUND FEATURE TO THE USER
320
MORE FEATURES IN DATABASE?
YES
NO
324
END
326
READ NEXT FEATURE IN DATABASE

FIGURE 6